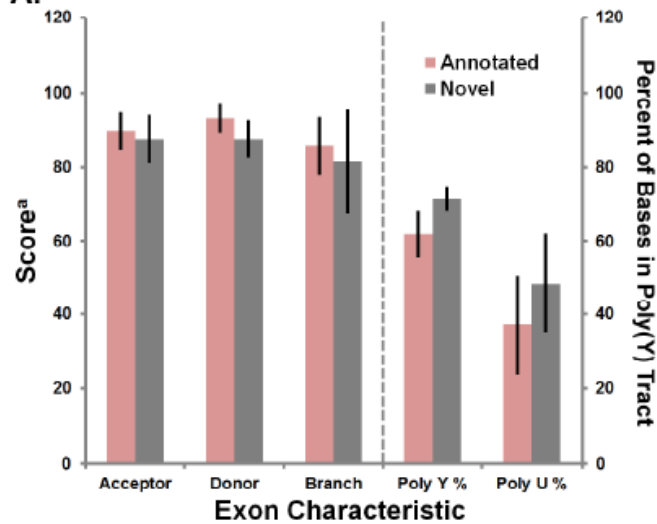


Figure S2 – *HTR2A* Exon Characteristics.

A. Annotated vs. Novel Exon Characteristics



B. Annotated vs. Novel Exon Characteristics

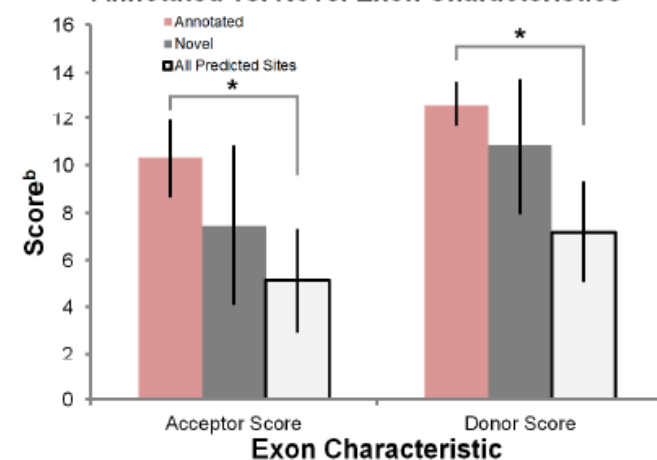


Figure S2. (A) Splice acceptor, splice donor, and branch site scores did not significantly differ across annotated and novel exons in *HTR2A*. The enrichment of polypyrimidines [Poly(Y)] in the Poly(Y) tract, defined as bases -5 to -40 upstream of the exon, also did not significantly differ. (B) Using a different *in silico* prediction program, we again see no significant difference between splice acceptor or splice donor scores for annotated versus novel exons. On average, annotated exons did score significantly higher than the all predicted sites in the *HTR2A* gene locus ($*p < 0.05$). ^aScores predicted by the Human Splicing Finder (<http://www.umd.be/HSF/>; Desmet et al., 2009). ^bScores predicted by the Alternative Splice Site Predictor (<http://wangcomputing.com/assp/index.html>; Wang et al., 2006). Error bars depict standard deviation.